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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=6; day=9; hr=12; min=53; sec=32; ms=720;]

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Reviewer Comments:

<140> 10633484

<141> 2008-05-14

<150> EP 02017313.4

<151> 2002-08-01

<160> 8

<170> PatentIn version 3.3

<220>

<221> misc_feature

<222> (1)..(173)

<223> p14arf, Swissprot Accession Q8N726

<400> 14

The above is a sample of invalid <160> response 8, in addition to part of the last sequence id# 14 which appears at the end of the sequence. Please correct <160> response to 14, which is the total number of sequences that appear.

Application No: 10633484 Version No: 2.0

Input Set:

Output Set:

Started: 2008-05-14 15:41:58.445
Finished: 2008-05-14 15:41:59.475
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 30 ms
Total Warnings: 0
Total Errors: 1
No. of SeqIDs Defined: 8
Actual SeqID Count: 14

Error code	Error Description
E 252	Calc# of Seq. differs from actual; 8 seqIds defined; count=14

SEQUENCE LISTING

<110> Rudiger Ridder, et.al.

<120> Method for solution based diagnosis

<130> 05033.0003.00US00

<140> 10633484

<141> 2008-05-14

<150> EP 02017313.4

<151> 2002-08-01

<160> 8

<170> PatentIn version 3.3

<210> 1

<211> 745

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(745)

<223> gamma-Catenin, Swissprot Accession Q86W21

<400> 1

Met Glu Val Met Asn Leu Met Glu Gln Pro Ile Lys Val Thr Glu Trp
1 5 10 15

Gln Gln Thr Tyr Thr Tyr Asp Ser Gly Ile His Ser Gly Ala Asn Thr
20 25 30

Cys Val Pro Ser Val Ser Ser Lys Gly Ile Met Glu Glu Asp Glu Ala
35 40 45

Cys Gly Arg Gln Tyr Thr Leu Lys Lys Thr Thr Thr Tyr Thr Gln Gly
50 55 60

Val Pro Pro Ser Gln Gly Asp Leu Glu Tyr Gln Met Ser Thr Thr Ala
65 70 75 80

Arg Ala Lys Arg Val Arg Glu Ala Met Cys Ser Gly Val Ser Gly Glu
85 90 95

Asp Ser Ser Leu Leu Leu Ala Thr Gln Val Glu Gly Gln Ala Thr Asn

100

105

110

Leu Gln Arg Leu Ala Glu Pro Ser Gln Leu Leu Lys Ser Ala Ile Val
115 120 125

His Leu Ile Asn Tyr Gln Asp Asp Ala Glu Leu Ala Thr Arg Ala Leu
130 135 140

Pro Glu Leu Thr Lys Leu Leu Asn Asp Glu Asp Pro Val Val Val Thr
145 150 155 160

Lys Ala Ala Met Ile Val Asn Gln Leu Ser Lys Lys Glu Ala Ser Arg
165 170 175

Arg Ala Leu Met Gly Ser Pro Gln Leu Val Ala Ala Val Val Arg Thr
180 185 190

Met Gln Asn Thr Ser Asp Leu Asp Thr Ala Arg Cys Thr Thr Ser Ile
195 200 205

Leu His Asn Leu Ser His His Arg Glu Gly Leu Leu Ala Ile Phe Lys
210 215 220

Ser Gly Gly Ile Pro Ala Leu Val Arg Met Leu Ser Ser Pro Val Glu
225 230 235 240

Ser Val Leu Phe Tyr Ala Ile Thr Thr Leu His Asn Leu Leu Leu Tyr
245 250 255

Gln Glu Gly Ala Lys Met Ala Val Arg Leu Ala Asp Gly Leu Gln Lys
260 265 270

Met Val Pro Leu Leu Asn Lys Asn Asn Pro Lys Phe Leu Ala Ile Thr
275 280 285

Thr Asp Cys Leu Gln Leu Leu Ala Tyr Gly Asn Gln Glu Ser Lys Leu
290 295 300

Ile Ile Leu Ala Asn Gly Gly Pro Gln Ala Leu Val Gln Ile Met Arg
305 310 315 320

Asn Tyr Ser Tyr Glu Lys Leu Leu Trp Thr Thr Ser Arg Val Leu Lys
325 330 335

Val Leu Ser Val Cys Pro Ser Asn Lys Pro Ala Ile Val Glu Ala Gly
340 345 350

Gly Met Gln Ala Leu Gly Lys His Leu Thr Ser Asn Ser Pro Arg Leu
355 360 365

Val Gln Asn Cys Leu Trp Thr Leu Arg Asn Leu Ser Asp Val Ala Thr
370 375 380

Lys Gln Glu Gly Leu Glu Ser Val Leu Lys Ile Leu Val Asn Gln Leu
385 390 395 400

Ser Val Asp Asp Val Asn Val Leu Thr Cys Ala Thr Gly Thr Leu Ser
405 410 415

Asn Leu Thr Cys Asn Asn Ser Lys Asn Lys Thr Leu Val Thr Gln Asn
420 425 430

Ser Gly Val Glu Ala Leu Ile His Ala Ile Leu Arg Ala Gly Asp Lys
435 440 445

Asp Asp Ile Thr Glu Pro Ala Val Cys Ala Leu Arg His Leu Thr Ser
450 455 460

Arg His Pro Glu Ala Glu Met Ala Gln Asn Ser Val Arg Leu Asn Tyr
465 470 475 480

Gly Ile Pro Ala Ile Val Lys Leu Leu Asn Gln Pro Asn Gln Trp Pro
485 490 495

Leu Val Lys Ala Thr Ile Gly Leu Ile Arg Asn Leu Ala Leu Cys Pro
500 505 510

Ala Asn His Ala Pro Leu Gln Glu Ala Ala Val Ile Pro Arg Leu Val
515 520 525

Gln Leu Leu Val Lys Ala His Gln Asp Ala Gln Arg His Val Ala Ala
530 535 540

Gly Thr Gln Gln Pro Tyr Thr Asp Gly Val Arg Met Glu Glu Ile Val
545 550 555 560

Glu Gly Cys Thr Gly Ala Leu His Ile Leu Ala Arg Asp Pro Met Asn
565 570 575

Arg Met Glu Ile Phe Arg Leu Asn Thr Ile Pro Leu Phe Val Gln Leu
580 585 590

Leu Tyr Ser Ser Val Glu Asn Ile Gln Arg Val Ala Ala Gly Val Leu
595 600 605

Cys Glu Leu Ala Gln Asp Lys Glu Ala Ala Asp Ala Ile Asp Ala Glu
610 615 620

Gly Ala Ser Ala Pro Leu Met Glu Leu Leu His Ser Arg Asn Glu Gly
625 630 635 640

Thr Ala Thr Tyr Ala Ala Ala Val Leu Phe Arg Ile Ser Glu Asp Lys
645 650 655

Asn Pro Asp Tyr Arg Lys Arg Val Ser Val Glu Leu Thr Asn Ser Leu
660 665 670

Phe Lys His Asp Pro Ala Ala Trp Glu Ala Ala Gln Ser Met Ile Pro
675 680 685

Ile Asn Glu Pro Tyr Gly Asp Asp Leu Asp Ala Thr Tyr Arg Pro Met
690 695 700

Tyr Ser Ser Asp Val Pro Leu Asp Pro Leu Glu Met His Met Asp Met
705 710 715 720

Asp Gly Asp Tyr Pro Ile Asp Thr Tyr Ser Asp Gly Leu Arg Pro Pro
725 730 735

Tyr Pro Thr Ala Asp His Met Leu Ala
740 745

<210> 2
<211> 314
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)..(314)

<223> Ep-Cam, Swissprot Accession P16422

<400> 2

Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
1 5 10 15

Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
20 25 30

Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
35 40 45

Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
50 55 60

Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
65 70 75 80

Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
85 90 95

Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
100 105 110

Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
115 120 125

Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
130 135 140

Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
145 150 155 160

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
165 170 175

Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
180 185 190

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
195 200 205

Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
210 215 220

Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
225 230 235 240

Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
245 250 255

Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
260 265 270

Val Val Val Val Met Ala Val Val Ala Gly Ile Val Val Leu Val Ile
275 280 285

Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
290 295 300

Met Gly Glu Met His Arg Glu Leu Asn Ala
305 310

<210> 3
<211> 882
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(882)
<223> E-Cadherin, Swissprot Accession P12830

<400> 3

Met Gly Pro Trp Ser Arg Ser Leu Ser Ala Leu Leu Leu Leu Gln
1 5 10 15

Val Ser Ser Trp Leu Cys Gln Glu Pro Glu Pro Cys His Pro Gly Phe
20 25 30

Asp Ala Glu Ser Tyr Thr Phe Thr Val Pro Arg Arg His Leu Glu Arg
35 40 45

Gly Arg Val Leu Gly Arg Val Asn Phe Glu Asp Cys Thr Gly Arg Gln
50 55 60

Arg Thr Ala Tyr Phe Ser Leu Asp Thr Arg Phe Lys Val Gly Thr Asp
65 70 75 80

Gly Val Ile Thr Val Lys Arg Pro Leu Arg Phe His Asn Pro Gln Ile
85 90 95

His Phe Leu Val Tyr Ala Trp Asp Ser Thr Tyr Arg Lys Phe Ser Thr
100 105 110

Lys Val Thr Leu Asn Thr Val Gly His His His Arg Pro Pro Pro His
115 120 125

Gln Ala Ser Val Ser Gly Ile Gln Ala Glu Leu Leu Thr Phe Pro Asn
130 135 140

Ser Ser Pro Gly Leu Arg Arg Gln Lys Arg Asp Trp Val Ile Pro Pro
145 150 155 160

Ile Ser Cys Pro Glu Asn Glu Lys Gly Pro Phe Pro Lys Asn Leu Val
165 170 175

Gln Ile Lys Ser Asn Lys Asp Lys Glu Gly Lys Val Phe Tyr Ser Ile
180 185 190

Thr Gly Gln Gly Ala Asp Thr Pro Pro Val Gly Val Phe Ile Ile Glu
195 200 205

Arg Glu Thr Gly Trp Leu Lys Val Thr Glu Pro Leu Asp Arg Glu Arg
210 215 220

Ile Ala Thr Tyr Thr Leu Phe Ser His Ala Val Ser Ser Asn Gly Asn
225 230 235 240

Ala Val Glu Asp Pro Met Glu Ile Leu Ile Thr Val Thr Asp Gln Asn
245 250 255

Asp Asn Lys Pro Glu Phe Thr Gln Glu Val Phe Lys Gly Ser Val Met
260 265 270

Glu Gly Ala Leu Pro Gly Thr Ser Val Met Glu Val Thr Ala Thr Asp
275 280 285

Ala Asp Asp Asp Val Asn Thr Tyr Asn Ala Ala Ile Ala Tyr Thr Ile

290

295

300

Leu Ser Gln Asp Pro Glu Leu Pro Asp Lys Asn Met Phe Thr Ile Asn
305 310 315 320

Arg Asn Thr Gly Val Ile Ser Val Val Thr Thr Gly Leu Asp Arg Glu
325 330 335

Ser Phe Pro Thr Tyr Thr Leu Val Val Gln Ala Ala Asp Leu Gln Gly
340 345 350

Glu Gly Leu Ser Thr Thr Ala Thr Ala Val Ile Thr Val Thr Asp Thr
355 360 365

Asn Asp Asn Pro Pro Ile Phe Asn Pro Thr Thr Tyr Lys Gly Gln Val
370 375 380

Pro Glu Asn Glu Ala Asn Val Val Ile Thr Thr Leu Lys Val Thr Asp
385 390 395 400

Ala Asp Ala Pro Asn Thr Pro Ala Trp Glu Ala Val Tyr Thr Ile Leu
405 410 415

Asn Asp Asp Gly Gly Gln Phe Val Val Thr Thr Asn Pro Val Asn Asn
420 425 430

Asp Gly Ile Leu Lys Thr Ala Lys Gly Leu Asp Phe Glu Ala Lys Gln
435 440 445

Gln Tyr Ile Leu His Val Ala Val Thr Asn Val Val Pro Phe Glu Val
450 455 460

Ser Leu Thr Thr Ser Thr Ala Thr Val Thr Val Asp Val Leu Asp Val
465 470 475 480

Asn Glu Ala Pro Ile Phe Val Pro Pro Glu Lys Arg Val Glu Val Ser
485 490 495

Glu Asp Phe Gly Val Gly Gln Glu Ile Thr Ser Tyr Thr Ala Gln Glu
500 505 510

Pro Asp Thr Phe Met Glu Gln Lys Ile Thr Tyr Arg Ile Trp Arg Asp
515 520 525

Thr Ala Asn Trp Leu Glu Ile Asn Pro Asp Thr Gly Ala Ile Ser Thr
530 535 540

Arg Ala Glu Leu Asp Arg Glu Asp Phe Glu His Val Lys Asn Ser Thr
545 550 555 560

Tyr Thr Ala Leu Ile Ile Ala Thr Asp Asn Gly Ser Pro Val Ala Thr
565 570 575

Gly Thr Gly Thr Leu Leu Leu Ile Leu Ser Asp Val Asn Asp Asn Ala
580 585 590

Pro Ile Pro Glu Pro Arg Thr Ile Phe Phe Cys Glu Arg Asn Pro Lys
595 600 605

Pro Gln Val Ile Asn Ile Ile Asp Ala Asp Leu Pro Pro Asn Thr Ser
610 615 620

Pro Phe Thr Ala Glu Leu Thr His Gly Ala Ser Ala Asn Trp Thr Ile
625 630 635 640

Gln Tyr Asn Asp Pro Thr Gln Glu Ser Ile Ile Leu Lys Pro Lys Met
645 650 655

Ala Leu Glu Val Gly Asp Tyr Lys Ile Asn Leu Lys Leu Met Asp Asn
660 665 670

Gln Asn Lys Asp Gln Val Thr Thr Leu Glu Val Ser Val Cys Asp Cys
675 680 685

Glu Gly Ala Ala Gly Val Cys Arg Lys Ala Gln Pro Val Glu Ala Gly
690 695 700

Leu Gln Ile Pro Ala Ile Leu Gly Ile Leu Gly Gly Ile Leu Ala Leu
705 710 715 720

Leu Ile Leu Ile Leu Leu Leu Leu Leu Phe Leu Arg Arg Arg Ala Val
725 730 735

Val Lys Glu Pro Leu Leu Pro Pro Glu Asp Asp Thr Arg Asp Asn Val
740 745 750

Tyr Tyr Tyr Asp Glu Glu Gly Gly Gly Glu Glu Asp Gln Asp Phe Asp
755 760 765

Leu Ser Gln Leu His Arg Gly Leu Asp Ala Arg Pro Glu Val Thr Arg
770 775 780

Asn Asp Val Ala Pro Thr Leu Met Ser Val Pro Arg Tyr Leu Pro Arg
785 790 795 800

Pro Ala Asn Pro Asp Glu Ile Gly Asn Phe Ile Asp Glu Asn Leu Lys
805 810 815

Ala Ala Asp Thr Asp Pro Thr Ala Pro Pro Tyr Asp Ser Leu Leu Val
820 825 830

Phe Asp Tyr Glu Gly Ser Gly Ser Glu Ala Ala Ser Leu Ser Ser Leu
835 840 845

Asn Ser Ser Glu Ser Asp Lys Asp Gln Asp Tyr Asp Tyr Leu Asn Glu
850 855 860

Trp Gly Asn Arg Phe Lys Lys Leu Ala Asp Met Tyr Gly Gly Gly Glu
865 870 875 880

Asp Asp

<210> 4
<211> 906
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(906)
<223> Alpha-1 Catenin, Swissprot Accession P35221

<400> 4

Met Thr Ala Val His Ala Gly Asn Ile Asn Phe Lys Trp Asp Pro Lys
1 5 10 15

Ser Leu Glu Ile Arg Thr Leu Ala Val Glu Arg Leu Leu Glu Pro Leu
20